Analysis of dynamic changes in the meat microbiota during temperature exposures - a novel method to estimate temperature history and pathogen growth in meat

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P27: Analysis of dynamic changes in the meat microbiota during temperature exposures - a novel method to estimate temperature history and pathogen growth in meat

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Outbreaks of food-borne zoonoses caused by pathogens such as *Salmonella*, *E. coli* or *Yersinia enterocolitica* are often associated with the consumption of contaminated meat. Temperatures in the cold chain (< 5 °C) are considered crucial in the prevention of pathogen growth in meat. However, handling of fresh meat is often performed at temperatures above 5 °C and without temperature control. Moreover, recent monitoring data from fresh meat processing facilities indicate growth of Salmonella. Thus, there is a need for methods that can disclose how temperature exposure influences the occurrence of pathogens in the meat chain from slaughter, through processing, to retail.

The overall objective of this project is to develop a method that enables an estimation of the temperature exposure of meat from slaughter to any chosen point in the meat chain. As a novel approach, this will be done by analyzing the dynamic changes in the meat microbiota during varied temperature exposures. The background flora comprises many bacterial species with different growth potential. Thus, we hypothesize that time and temperature exposure will lead to systematic changes in certain parts of the background flora. Based on the composition of the flora, the study aims to provide a time/temperature exposure estimate for fresh meat, preferably given as a standardized measure (index). By adding a predictive modelling approach, this will allow for an estimation of the expected pathogen growth (e.g. Salmonella). Systematic changes in the meat microbiota will be investigated by 16S rDNA pyrosequencing, or a similar methodology. This novel approach will presumably contribute to the understanding of how meat hygiene and temperature exposure affect food safety. If successful, it will potentially provide a new tool for meat safety control in fresh meat production lines. Results describing microbial sub-populations based on the chosen sequencing approach will be presented.

P28: Antimicrobial resistance of *Staphylococcus epidermidis* isolated in Tlemcen "Algeria"

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Nosocomial infections are a real public health problem. We are interested in finding the species *Staphylococcus epidermidis* in the trauma unit, knowing that it is more resistant to antibiotics and met more and more in a variety of infections in hospitals. Therefore, we took 265 samples in our unit at the University Hospital of Tlemcen, which consisted of nasal ports (48h before surgery) and surgical wounds (4 days after surgery) in operated patients. Using the API STAPH system, 75 strains of *S. epidermidis* were identified. Drug resistance profiles, using the NCCLS standards, reveals a rate of 90% multiresistant strains, mainly to ampicillin (100%), penicillin (100%), oxacillin (93.33%). We also found that 66.66% of the strains were resistant to erythromycin and 33.33% resistant to vancomycin, and only one strain was sensitive to oxacillin.

P29: A sticky business: The differential role of extracellular DNA, proteins and polysaccharides in the initial adhesion of Staphylococcus spp.

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The diversity in mechanisms for bacterial attachment and biofilm formation is the overarching challenge for development of strategies to combat biofilms. Understanding the quantitative contribution of different cell surface adhesins to biofilm formation is therefore necessary for designing new approaches to biofilm prevention. In this study, we combine microfluidic flowcell studies with single-cell analyses to understand how polysaccharides, extracellular DNA (eDNA), and proteins contribute to bacterial adhesion and aggregation on abiotic surfaces. We quantified initial adhesion, cell aggregation, and single-cell adhesion forces of *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *Staphylococcus xylosus* in the presence and absence of DNase, dispersin, or subtilisin, which cleave extracellular DNA, polysaccharides and proteins, respectively. Our results indicate a differential role of these macromolecules in the